

SEQUENCE LISTING

<110> Lee, Se-Jin
McPherron, Alexandra C.

<120> GROWTH DIFFERENTIATION FACTOR RECEPTORS,
AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

<130> JHU1470-2

<150> 09/485,046

<151> 2000-01-31

<150> PCT/US98/15598

<151> 1998-07-28

<150> 60/054,461

<151> 1997-08-01

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Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
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Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val	
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<213> Homo sapiens

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 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
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 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
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 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu

115 120 125
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 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
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 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
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 Met Met Gln Lys
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 ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc 163
 Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly
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 Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys
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 gag ggg ctg tgt aat gca tgt gcg tgg aga caa aac acg agg tac tcc 259
 Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser
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Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg	
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Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp	
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Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr	
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gaa aca atc att acc atg cct aca gag tct gac ttt cta atg caa gcg	499
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala	
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Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln	
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Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro	
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Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp	
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Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His	
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 Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys
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<213> Mus musculus

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 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
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 65 70 75 80
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 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
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 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
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 Leu Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
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 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
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 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
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 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
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 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
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 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
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<220>

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<222> (1)...(1128)

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48

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96

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Thr	Arg	Tyr	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys		
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Leu	Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln		
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Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr		
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Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val		
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acc	ttc	cca	gga	cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc		768
Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val		
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 aaa tat ccg cat act cat ctt gtg cac caa gca aac ccc aga ggc tcg 1008
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
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 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
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 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
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 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
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 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
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 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
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 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
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Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr	
35 40 45	
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Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
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cgc ctg gaa caa gca cct aac att agc agg gac gtt att aag cag ctt	240
Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu	
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Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val	
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Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
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Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	
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Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
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Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
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Ile Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr	
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Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg	
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Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
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Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
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 340 345 350

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 Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg
 50 55 60
 Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu Leu
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 Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala
 100 105 110
 Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Val
 115 120 125
 Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys
 130 135 140
 Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg
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 Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile
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 Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys
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 Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys
 195 200 205
 Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile
 210 215 220
 Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr Phe
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 Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg Val
 245 250 255
 Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp
 260 265 270
 Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
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 Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr
 305 310 315 320

Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly
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 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
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 cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
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 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
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 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
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 145 150 155 160
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Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val		
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Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala		
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Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
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Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
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Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
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Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val	
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Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu	
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Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
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 260 265 270

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 275 280 285

gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat 912
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 290 295 300

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 325 330 335

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 Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
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 Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
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Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
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 Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu
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 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 13

<211> 1128

<212> DNA

<213> Porcine

<220>

<221> CDS

<222> (1)...(1125)

<400> 13

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Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile	
1 5 10 15	
gtt gct ggt ccc gtg gat ctg aat gag aac agc gag caa aag gaa aat	96
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	
20 25 30	
gtg gaa aaa gag ggg ctg tgt aat gca tgt atg tgg aga caa aac act	144
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr	
35 40 45	
aaa tct tca aga cta gaa gcc ata aaa att caa atc ctc agt aaa ctt	192
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	
cgc ctg gaa aca gct cct aac att agc aaa gat gct ata aga caa ctt	240

Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
65					70					75					80	
ttg	ccc	aaa	gct	cct	cca	ctc	cgg	gaa	ctg	att	gat	cag	tac	gat	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
			85						90					95		
cag	aga	gat	gac	agc	agt	gat	ggc	tcc	ttg	gaa	gat	gat	gat	tat	cac	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105						110		
gct	acg	acg	gaa	acg	atc	att	acc	atg	cct	aca	gag	tct	gat	ctt	cta	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
			115				120						125			
atg	caa	gtg	gaa	gga	aaa	ccc	aaa	tgc	tgc	ttc	ttt	aaa	ttt	agc	tct	432
Met	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135							140			
aaa	ata	caa	tac	aat	aaa	gta	gta	aag	gcc	caa	ctg	tgg	ata	tat	ctg	480
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
aga	ccc	gtc	aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	528
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	act	gga	atc	cga	tct	ctg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	att	tgg	cag	agc	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200						205				
aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	caa	cct	gaa	tcc	aac	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215						220				
att	gaa	atc	aaa	gct	tta	gat	gag	aat	ggc	cat	gat	ctt	gct	gta	acc	720
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
ttc	cca	gga	cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc	aag	768
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
gta	aca	gac	aca	cca	aaa	aga	tcc	agg	aga	gat	ttt	gga	ctc	gac	tgt	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gat	gag	cac	tca	aca	gaa	tct	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
			275				280					285				
gat	ttt	gaa	gct	ttt	gga	tgg	gac	tgg	att	att	gca	ccc	aaa	aga	tat	912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aag	gcc	aat	tac	tgc	tct	gga	gag	tgt	gaa	ttt	gta	ttt	tta	caa	aaa	960

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320

tac cct cac act cat ctt gtg cac caa gca aac ccc aga ggt tca gca 1008
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335

ggc ccc tgc tgt act ccc aca aag atg tct cca atc aat atg cta tat 1056
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta 1104
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365

gta gat cgc tgt ggg tgc tca tga 1128
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 14

<211> 375

<212> PRT

<213> Porcine

<400> 14

Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile
 1 5 10 15
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

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Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
    275                      280                      285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
    290                      295                      300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
    305                      310                      315                      320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
    325                      330                      335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
    340                      345                      350
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
    355                      360                      365
Val Asp Arg Cys Gly Cys Ser
    370                      375

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<210> 15
 <211> 1128
 <212> DNA
 <213> Ovine

<220>
 <221> CDS
 <222> (1)...(1125)

<400> 15

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atg caa aaa ctg caa atc ttt gtt tat att tac cta ttt atg ctg ctt      48
Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
  1                      5                      10                      15

gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat      96
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
    20                      25                      30

gtg gaa aaa aag ggg ctg tgt aat gca tgc ttg tgg aga caa aac aat      144
Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
    35                      40                      45

aaa tcc tca aga cta gaa gcc ata aaa atc caa atc ctc agt aag ctt      192
Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
    50                      55                      60

cgc ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt      240
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
    65                      70                      75                      80

ttg ccc aag gct cct cca ctc cgg gaa ctg att gat cag tac gat gtc      288
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
    85                      90                      95

cag aga gat gac agc agc gac ggc tcc ttg gaa gac gat gac tac cac      336
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
    100                      105                      110

gtt acg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta      384
Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
    115                      120                      125

gca gaa gtg caa gaa aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct      432
Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
    130                      135                      140

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aag ata caa cac aat aaa gta gta aag gcc caa ctg tgg ata tat ctg Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu 145 150 155 160	480
aga cct gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu 165 170 175	528
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu 180 185 190	576
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val 195 200 205	624
aag aca gtg ttg caa aac tgg ctc aaa caa cct gaa tcc aac tta ggc Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly 210 215 220	672
att gaa atc aaa gct tta gat gag aat ggt cat gat ctt gct gta acc Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr 225 230 235 240	720
ttc cca gaa cca gga gaa gaa gga ctg aat cct ttt tta gaa gtc aag Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys 245 250 255	768
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys 260 265 270	816
gat gag cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val 275 280 285	864
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr 290 295 300	912
aag gcc aat tac tgc tct gga gaa tgt gaa ttt tta ttt ttg caa aag Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys 305 310 315 320	960
tat cct cat acc cat ctt gtg cac caa gca aac ccc aaa ggt tca gcc Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala 325 330 335	1008
ggc cct tgc tgt act cct aca aag atg tct cca att aat atg cta tat Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr 340 345 350	1056
ttt aat ggc aaa gaa caa ata ata tat ggg aag att cca ggc atg gta Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val 355 360 365	1104
gta gat cgc tgt ggg tgc tca tga Val Asp Arg Cys Gly Cys Ser 370 375	1128

<210> 16
 <211> 375
 <212> PRT
 <213> Ovine

<400> 16

Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
 1 5 10 15
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
 35 40 45
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 17
 <211> 1128
 <212> DNA

<213> Meleagris gallopavo

<220>

<221> CDS

<222> (1)...(1125)

<400> 17

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Met	Gln	Lys	Leu	Ala	Val	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Gln	Ile	
1				5					10					15		

tta	gtt	cat	ccg	gtg	gct	ctt	gat	ggc	agt	agt	cag	ccc	aca	gag	aac	96
Leu	Val	His	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
			20					25					30			

gct	gaa	aaa	gac	gga	ctg	tgc	aat	gct	tgc	acg	tgg	aga	cag	aat	act	144
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35					40					45				

aaa	tcc	tcc	aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agc	aaa	ctg	192
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					

cgc	ctg	gaa	caa	gca	cct	aac	att	agc	agg	gac	gtt	att	aaa	caa	ctt	240
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
65					70				75					80		

tta	ccc	aaa	gct	cct	ccg	ctg	cag	gaa	ctg	att	gat	cag	tat	gac	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		

cag	aga	gac	gac	agt	agc	gat	ggc	tct	ttg	gaa	gac	gat	gac	tat	cat	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100				105						110			

gcc	aca	acc	gaa	acg	att	atc	aca	atg	cct	acg	gag	tct	gat	ttt	ctt	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				

gta	caa	atg	gag	gga	aaa	cca	aaa	tgt	tgc	ttc	ttt	aag	ttt	agc	tct	432
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
		130					135				140					

aaa	ata	caa	tat	aac	aaa	gta	gta	aag	gca	caa	tta	tgg	ata	tac	ttg	480
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	

agg	caa	gtc	caa	aaa	cct	aca	acg	gtg	ttt	gtg	cag	atc	ctg	aga	ctc	528
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		

att	aaa	ccc	atg	aaa	gac	ggg	aca	aga	tat	act	gga	att	cga	tct	ttg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185						190		

aaa	ctt	gac	atg	aac	cca	ggc	act	ggg	atc	tgg	cag	agt	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200					205					

aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aat	tta	ggc	672
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Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210                215                220

atc gaa ata aaa gct ttt gat gag aat gga cga gat ctt gct gta aca      720
Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
225                230                235                240

ttc cca gga cca ggt gaa gat gga ctg aac cca ttt tta gag gtc aga      768
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
                245                250                255

gtt aca gac aca cca aaa cgg tcc cgc aga gat ttt ggc ctt gac tgc      816
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
                260                265                270

gac gag cac tca acg gaa tct cga tgt tgt cgc tac ccg ctg aca gtg      864
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
                275                280                285

gat ttt gaa gct ttt gga tgg gac tgg att ata gca cct aaa aga tac      912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
                290                295                300

aaa gcc aat tac tgc tct gga gaa tgt gaa ttc gta ttt cta cag aaa      960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
305                310                315                320

tac ccg cac act cac ctg gta cac caa gca aat cca aga ggc tca gca      1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
                325                330                335

ggc cct tgc tgc aca ccc acc aag atg tcc cct ata aac atg ctg tat      1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
                340                345                350

ttc aat gga aaa gaa caa ata ata tat gga aag ata cca gcc atg gtt      1104
Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
                355                360                365

gta gat cgt tgc ggg tgc tca tga      1128
Val Asp Arg Cys Gly Cys Ser
                370                375

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<210> 18

<211> 375

<212> PRT

<213> Meleagris gallopavo

<400> 18

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                20                25                30
Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
                35                40                45
Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
                50                55                60
Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
65                70                75                80

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Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 19

<211> 1125

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (1)... (1122)

<400> 19

atg	cat	ttt	aca	cag	gtt	tta	att	tct	cta	agt	gta	tta	att	gca	tgt	48
Met	His	Phe	Thr	Gln	Val	Leu	Ile	Ser	Leu	Ser	Val	Leu	Ile	Ala	Cys	
1				5					10					15		

ggt	cca	gtg	ggt	tat	gga	gat	ata	acg	gcg	cac	cag	cag	cct	tcc	aca	96
Gly	Pro	Val	Gly	Tyr	Gly	Asp	Ile	Thr	Ala	His	Gln	Gln	Pro	Ser	Thr	
		20						25					30			

gcc	acg	gag	gaa	agc	gag	ctg	tgt	tcc	aca	tgt	gag	ttc	aga	caa	cac	144
Ala	Thr	Glu	Ser	Glu	Leu	Cys	Ser	Thr	Cys	Glu	Phe	Arg	Gln	His		
		35				40					45					

agc aag ctg atg aga ctg cat gcc atc aag tcc caa att ctt agc aaa	192
Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys	
50 55 60	
ctc cga ctc aag cag gct cca aac atc agc cgg gac gtg gtc aag cag	240
Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln	
65 70 75 80	
ctg tta ccc aaa gca ccg cct ttg caa caa ctt ctg gat cag tac gat	288
Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp	
85 90 95	
gtt tta gga gat gac agt aag gat gga gct gtg gaa gag gac gat gaa	336
Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu	
100 105 110	
cat gcc acc aca gag acc atc atg acc atg gcc aca gaa cct gac ccc	384
His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro	
115 120 125	
att gtt caa gta gat cgg aaa ccg aag tgt tgc ttt ttc tcc ttc agt	432
Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser	
130 135 140	
ccg aag atc caa gcg aac ccg atc gta aga gcg cag ctc tgg gtt cat	480
Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His	
145 150 155 160	
ctg aga ccg gcg gag gag gcg acc acc gtc ttc tta cag ata tct cgg	528
Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg	
165 170 175	
ctg atg ccc gtt aag gac gga gga aga cac cga ata cga tcc ctg aaa	576
Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys	
180 185 190	
tatc gac gtg aac gca gga gtc acg tct tgg cag agt ata gac gta aag	624
Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys	
195 200 205	
cag gtg ctc acg gtg tgg tta aaa caa ccg gag acc aac cga ggc atc	672
Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile	
210 215 220	
gag att aac gca tat gac gcg aag gga aac gac ttg gcc gtc act tca	720
Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser	
225 230 235 240	
acc gag act ggg gag gat gga ctg ctc ccc ttt atg gag gtg aaa ata	768
Thr Glu Thr Gly Glu Asp Gly Leu Leu Phe Met Glu Val Lys Ile	
245 250 255	
tca gag ggc cca aaa cga atc ccg agg gac tcc gga ctg gac tgc gat	816
Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp	
260 265 270	
gag aat tcc tca gag tct cgc tgc tgc agg tac cct ctc act gtg gac	864
Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp	
275 280 285	

ttc gag gac ttt ggc tgg gac tgg att att gct cca aaa cgc tat aag 912
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
 290 295 300

gcg aat tac tgt tca gga gaa tgc gac tac atg tac ctg cag aag tat 960
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr
 305 310 315 320

ccc cac acc cat ctg gtg aac aag gcc agt ccg aga gga acg gct ggg 1008
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly
 325 330 335

ccc tgc tgc act ccc acc aag atg tct ccc atc aac atg ctt tac ttt 1056
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350

aac ggc aaa gag cag atc atc tac ggc aag atc cct tcg atg gta gta 1104
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val
 355 360 365

gac cgc tgt ggc tgc tca tga 1125
 Asp Arg Cys Gly Cys Ser
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<210> 20

<211> 374

<212> PRT

<213> Danio rerio

<400> 20

Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys
 1 5 10 15
 Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr
 20 25 30
 Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His
 35 40 45
 Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln
 65 70 75 80
 Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp
 85 90 95
 Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu
 100 105 110
 His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro
 115 120 125
 Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser
 130 135 140
 Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His
 145 150 155 160
 Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg
 165 170 175
 Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys
 180 185 190
 Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys
 195 200 205
 Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile
 210 215 220

Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser
 225 230 235 240
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile
 245 250 255
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp
 260 265 270
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
 290 295 300
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr
 305 310 315 320
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
 370

<210> 21
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 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> Xaa = Any Amino Acid

<400> 21
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<210> 22
 <211> 4
 <212> PRT
 <213> Eukaryotes

<220>
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 <223> proteolytic processing site

<400> 22
 Arg Ser Arg Arg
 1

<210> 23
 <211> 4
 <212> PRT
 <213> Eukaryotes

<220>
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 <223> proteolytic processing site

<400> 23
Arg Ile Arg Arg
1

<210> 24
<211> 1393
<212> DNA
<213> Homo sapiens

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<222> (54)...(1274)
<223> GDF-11

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Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Leu Ala Leu Glu
5 10 15
ctg cgg ccc cgg ggg gag gcg gcc gag ggc ccc gcg gcg gcg gcg gcg 152
Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala Ala
20 25 30
gcg gcg gcg gcg gcg gca gcg gcg ggg gtc ggg ggg gag cgc tcc agc 200
Ala Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser Ser
35 40 45
cgg cca gcc ccg tcc gtg gcg ccc gag ccg gac ggc tgc ccc gtg tgc 248
Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val Cys
50 55 60 65
gtt tgg cgg cag cac agc cgc gag ctg cgc cta gag agc atc aag tcg 296
Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys Ser
70 75 80
cag atc ttg agc aaa ctg cgg ctc aag gag gcg ccc aac atc agc cgc 344
Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser Arg
85 90 95
gag gtg gtg aag cag ctg ctg ccc aag gcg ccg ccg ctg cag cag atc 392
Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Ile
100 105 110
ctg gac cta cac gac ttc cag ggc gac gcg ctg cag ccc gag gac ttc 440
Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp Phe
115 120 125
ctg gag gag gac gag tac cac gcc acc acc gag acc gtc att agc atg 488
Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser Met
130 135 140 145
gcc cag gag acg gac cca gca gta cag aca gat ggc agc cct ctc tgc 536
Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu Cys
150 155 160

tgc cat ttt cac ttc agc ccc aag gtg atg ttc aca aag gta ctg aag Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu Lys 165 170 175	584
gcc cag ctg tgg gtg tac cta cgg cct gta ccc cgc cca gcc aca gtc Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr Val 180 185 190	632
tac ctg cag atc ttg cga cta aaa ccc cta act ggg gaa ggg acc gca Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr Ala 195 200 205	680
ggg gga ggg ggc gga ggc cgg cgt cac atc cgt atc cgc tca ctg aag Gly Gly Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu Lys 210 215 220 225	728
att gag ctg cac tca cgc tca ggc cat tgg cag agc atc gac ttc aag Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe Lys 230 235 240	776
caa gtg cta cac agc tgg ttc cgc cag cca cag agc aac tgg ggc atc Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly Ile 245 250 255	824
gag atc aac gcc ttt gat ccc agt ggc aca gac ctg gct gtc acc tcc Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr Ser 260 265 270	872
ctg ggg ccg gga gcc gag ggg ctg cat cca ttc atg gag ctt cga gtc Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg Val 275 280 285	920
cta gag aac aca aaa cgt tcc cgg cgg aac ctg ggt ctg gac tgc gac Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys Asp 290 295 300 305	968
gag cac tca agc gag tcc cgc tgc tgc cga tat ccc ctc aca gtg gac Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp 310 315 320	1016
ttt gag gct ttc ggc tgg gac tgg atc atc gca cct aag cgc tac aag Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys 325 330 335	1064
gcc aac tac tgc tcc ggc cag tgc gag tac atg ttc atg caa aaa tat Ala Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys Tyr 340 345 350	1112
ccg cat acc cat ttg gtg cag cag gcc aat cca aga ggc tct gct ggg Pro His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala Gly 355 360 365	1160
ccc tgt tgt acc ccc acc aag atg tcc cca atc aac atg ctc tac ttc Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe 370 375 380 385	1208
aat gac aag cag cag att atc tac ggc aag atc cct ggc atg gtg gtg Asn Asp Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val Val 390 395 400	1256

gat cgc tgt ggc tgc tct taagtgggtc actacaagct gctggagcaa
 Asp Arg Cys Gly Cys Ser
 405

1304

agacttggtg ggtgggtaac ttaacctctt cacagaggat aaaaaatgct tgtgagtatg 1364
 acagaaggga ataaacaggc ttaaagggt 1393

<210> 25

<211> 407

<212> PRT

<213> Homo sapiens

<400> 25

Met	Val	Leu	Ala	Ala	Pro	Leu	Leu	Leu	Gly	Phe	Leu	Leu	Leu	Ala	Leu
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Glu	Leu	Arg	Pro	Arg	Gly	Glu	Ala	Ala	Glu	Gly	Pro	Ala	Ala	Ala	Ala
			20					25					30		
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Val	Gly	Gly	Glu	Arg	Ser
			35				40					45			
Ser	Arg	Pro	Ala	Pro	Ser	Val	Ala	Pro	Glu	Pro	Asp	Gly	Cys	Pro	Val
			50			55					60				
Cys	Val	Trp	Arg	Gln	His	Ser	Arg	Glu	Leu	Arg	Leu	Glu	Ser	Ile	Lys
65					70					75				80	
Ser	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Lys	Glu	Ala	Pro	Asn	Ile	Ser
				85					90					95	
Arg	Glu	Val	Val	Lys	Gln	Leu	Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Gln
			100					105						110	
Ile	Leu	Asp	Leu	His	Asp	Phe	Gln	Gly	Asp	Ala	Leu	Gln	Pro	Glu	Asp
			115				120						125		
Phe	Leu	Glu	Glu	Asp	Glu	Tyr	His	Ala	Thr	Thr	Glu	Thr	Val	Ile	Ser
			130			135					140				
Met	Ala	Gln	Glu	Thr	Asp	Pro	Ala	Val	Gln	Thr	Asp	Gly	Ser	Pro	Leu
145					150					155					160
Cys	Cys	His	Phe	His	Phe	Ser	Pro	Lys	Val	Met	Phe	Thr	Lys	Val	Leu
				165					170					175	
Lys	Ala	Gln	Leu	Trp	Val	Tyr	Leu	Arg	Pro	Val	Pro	Arg	Pro	Ala	Thr
			180				185						190		
Val	Tyr	Leu	Gln	Ile	Leu	Arg	Leu	Lys	Pro	Leu	Thr	Gly	Glu	Gly	Thr
			195				200					205			
Ala	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Arg	His	Ile	Arg	Ile	Arg	Ser	Leu
			210			215					220				
Lys	Ile	Glu	Leu	His	Ser	Arg	Ser	Gly	His	Trp	Gln	Ser	Ile	Asp	Phe
225					230					235					240
Lys	Gln	Val	Leu	His	Ser	Trp	Phe	Arg	Gln	Pro	Gln	Ser	Asn	Trp	Gly
				245					250					255	
Ile	Glu	Ile	Asn	Ala	Phe	Asp	Pro	Ser	Gly	Thr	Asp	Leu	Ala	Val	Thr
			260				265						270		
Ser	Leu	Gly	Pro	Gly	Ala	Glu	Gly	Leu	His	Pro	Phe	Met	Glu	Leu	Arg
			275				280					285			
Val	Leu	Glu	Asn	Thr	Lys	Arg	Ser	Arg	Arg	Asn	Leu	Gly	Leu	Asp	Cys
			290			295					300				
Asp	Glu	His	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
					310					315					320
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
				325					330					335	
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Glu	Tyr	Met	Phe	Met	Gln	Lys
			340				345						350		
Tyr	Pro	His	Thr	His	Leu	Val	Gln	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
			355				360					365			
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr

<210> 27
<211> 157

<212> PRT

<213> Salmon-1

<400> 27

Gln	Pro	Glu	Thr	Asn	Trp	Gly	Ile	Glu	Ile	Asn	Ala	Phe	Asp	Ser	Lys
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Gly	Asn	Asp	Leu	Ala	Val	Thr	Ser	Ala	Glu	Ala	Gly	Glu	Gly	Leu	Gln
			20					25					30		
Pro	Phe	Met	Glu	Val	Thr	Ile	Ser	Glu	Gly	Pro	Lys	Arg	Ser	Arg	Arg
		35					40					45			
Asp	Ser	Gly	Leu	Asp	Cys	Asp	Glu	Asn	Ser	Pro	Glu	Ser	Arg	Cys	Cys
	50				55					60					
Arg	Tyr	Pro	Leu	Thr	Val	Asp	Phe	Glu	Asp	Phe	Gly	Trp	Asp	Trp	Ile
65					70					75				80	
Ile	Ala	Pro	Lys	Arg	Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu
			85					90						95	
Tyr	Met	His	Leu	Gln	Lys	Tyr	Pro	His	Thr	His	Leu	Val	Asn	Lys	Ala
		100					105						110		
Asn	Pro	Arg	Gly	Thr	Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser
		115					120					125			
Pro	Ile	Asn	Met	Leu	Tyr	Phe	Asn	Arg	Lys	Glu	Gln	Ile	Ile	Tyr	Gly
	130					135					140				
Lys	Ile	Pro	Ser	Met	Val	Val	Asp	Arg	Cys	Gly	Cys	Ser			
145					150					155					

<210> 28

<211> 412

<212> DNA

<213> Salmon-2

<220>

<221> CDS

<222> (2) ... (409)

<400> 28

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Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val	
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aag att tcg gag ggc ccg aag cgc tcc agg aga gat tcg ggc ctg gac	97
Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp	
20 25 30	
tgt gat gag aac tcc ccc gag tcc cgc tgc tgc cgg tac ccc ctc acg	145
Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr	
35 40 45	
gtg gac ttt gaa gac ttt ggc tgg gac tgg att att gcc ccc aag cgc	193
Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg	
50 55 60	
tac aag gcc aac tac tgc tct ggt gag tgc gag tac atg cac ctg cag	241
Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln	
65 70 75 80	
aag tac ccc cac acc cac ctg gtg aac aag gct aac cct cgc ggc acc	289
Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr	
85 90 95	
gcg ggg ccc tgc tgc acc ccc acc aag atg tcc ccc atc aac atg ctc	337

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110

tac ttc aac cgc aaa gag cag atc atc tac ggc aag atc ccc tcc atg 385
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125

gtg gtg gac cgc tgc ggc tgc tcg tga 412
 Val Val Asp Arg Cys Gly Cys Ser
 130 135

<210> 29

<211> 136

<212> PRT

<213> Salmon-2

<400> 29

Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val
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 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp
 20 25 30
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 35 40 45
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 50 55 60
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln
 65 70 75 80
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr
 85 90 95
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125
 Val Val Asp Arg Cys Gly Cys Ser
 130 135